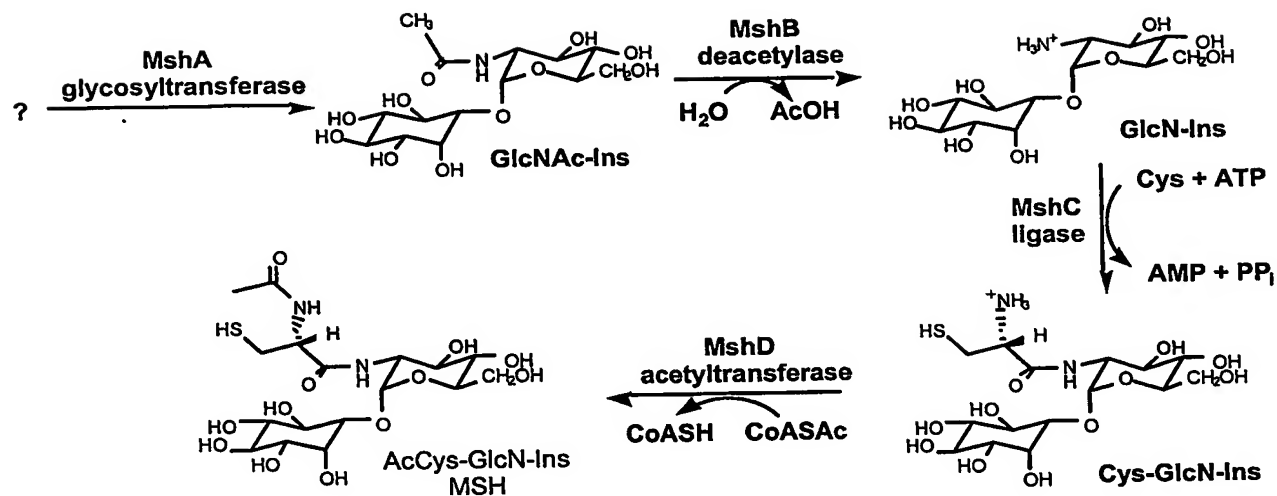


1/30

**Figure 1**

MshC nucleic acid sequence of *M. smegmatis*

ATGCAATCGTGGTCGGCACCGGCGATTCCGGTGGTTCCGGGACGTGGCCCTGCGCTG
CGCCTCTTCGACAGCGCTGATCGCCAGGTCCGGCCCGTCACACCGGGACCGACCGC
AACCATGTACGTGTGCGGCATCACCCATACGACGCGACCCATCTGGGTACGCCGC
GACCTATCTGACGTTTCGACCTGGTGCATCGCCTATGGCTCGACGCCGGACACACCGT
GCAGTACGTCCAGAACGTCACCGACGTGGACGACCCGTTGTTTCGAGCGTGCTGAGC
GCGACGGCATCGACTGGCGGACGCTGGGCGACCGCGAGACGCAGCTGTTCCGTGAG
GACATGGCCGCGTTGCGCGTGCTGCCCCGCGACGACTACGTCGCCGCGACCGACGC
GATCGCCGAGGTCGTCGAGATGGTCGAGAAGCTGCTGGCCTCGGGTGCGGCGTACA
TCGTCGAGGACGCCGAGTACCCCGACGTGTACTTCCGCGCCGACGCCACCGCGCAG
TTCGGGTACGAGTCCGGCTACGACCGCGACACCATGCTCACGTTGTTTCGCCGAACGC
GGCGGGGACCCGGACCGCCCGGGCAAGTCCGATCAACTCGACGCGTTGCTGTGGCG
CGCCGAGCGTCCTGGCGAGCCAGCTGGCCTTCGCCGTTTCGGCCGGGGCCGGCCCCG
GCTGGCACGTGGAATGTTTCGGCGATCGCCCTGACGCGGATCGGCACCGGCCTCGAC
ATCCAGGGCGGGCGGCAGCGACCTCATCTTCCCGCACACGAGTATTCGGCCGCGCA
CGCCGAATCCGTCACCGGTGAGCGACGATTCGCACGCCACTACGTGCACACCGGCA
TGATCGGCTGGGACGGCCACAAGATGAGCAAGAGCCGCGGCAACCTGGTCCTGGTG
TCGCAGTTGCGCGCCCAGGGCGTCGACCCGTCGGCGATCCGGCTCGGCCTGTTCTCC
GGGCACTACCGCGAGGACCGGTTCTGGAGCAACGAGGTTCTCGACGAGGCCAACGC
GCGACTCGCGCGGTGGCGCAGTGCCACCGCATTGCCCGAGGCGCCCGATGCGACCG
ACGTGATCGCGCGCGTCCGGCAGTACCTGGCCGATGACCTGGACACGCCGAAAGCG
CTTGCCGCACTCGATGGTTGGTGTACCGACGCGCTGTCCTACGGTGGGCACGACACC
GAGTCGCCGCGGCTCGTGGCCACCACCGTCGACGCGTTGCTGGGTGTGGACCTC

Figure 2A

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MshC amino acid sequence of *M. smegmatis* (PMshCMs)

MQSWSAPAIP VVPGRGPALR LFDSADRQVR PVTPGPTATM
YVCGITPYDA THLGHAATYL TFDLVHRLWL DAGHTVQYVQ
NVTDVDDPLF ERAERDGDW RTLGDRETQL FREDMAALRV
LPPHDYVAAT DAIAEVVEMV EKLLASGAAY IVEDAEYPDV
YFRADATAQF GYESGYDRDT MLTLFAERGG DPDRPGKSDQ
LDALLWRAER PGEPSWPSPF GRGRPGWHVE CSAIALTRIG TGLDIQGGGS
DLIFPHHEYS AAHAESVTGE RRFARHYVHT GMIGWDGHKM
SKSRGNLVLV SQLRAQGVDP SAIRLGLFSG HYREDRFWSN
EVLDEANARL ARWRSATALP EAPDATDVIA RVRQYLADDL
DTPKALAALD GWCTDALSYG GHDTESPRLV ATTVDALLGV DL (SEQ ID
NO: 2)

Figure 2B

4/30

>cysS2: 1242 bp - M. tuberculosis -

atgcagtcgtggtattgccaccggtccggtgttgccgggacgaggcccgagctacgg
ctgtacgacagcgccgaccggcaggtccgtccggtggcgcccgatctaaggccaccatg
tacgtctcggggatcacgccctacgacgccacgcatctgggccatgctgccacctatgtg
acgttcgacctgatccatcggtgtggctggatctcggtcatgaattgcactatgtccag
aacatcaccgacatcgacgatccactatttagcgcgcggtatcgcgacggtgtcgactgg
cgtgaccttggccaagccgaggtcgccctgttctgtgaggacatggcgggcgctgcggggtg
ctaccaccgcaagactacgtggggggccaccgaagcgattgctgaaatggtcgagctcatc
gaaaaaatgctggcgtgcggggcgccctatgtcatagaccgggaaatgggagagtaccag
gacatctacttcgcgctgacgccaccctgcagttcggctacgagtcagggtatgaccgt
gacaccatgctgcggctgtgcgaggaacgtggcgcgcatccgcggcgccccggcaagagc
gacgaactcgacgcgttgttgggcgggccgcgcgcccggtgagcccagctggccgtcc
ccgttcgggcctggccggccaggctggcatgtcgagtgcgagccatcgcgctcagtcgt
atcgggaagcgccctcgacatccaggcggtggtagcgatctgatcttccgaccacgag
ttcaccgctgcgcacgccgaatgtgtcagcggcgaaacggcgattcgcgggcactacgtg
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ctggtgtcggcgctgcgtgcgcaggacgttgagccatcggcggttcggctgggttgctc
gccgggacactaccgagccgatcggttctggagccagcaggtgcttgacgaggcgaccgcc
cggctgcaccgttggcgacccgaaccgcacttcccgggtccggccgcagttgacgtt
gtcgtcgggtgcgcccgtacctggccgacgatctcgatacgcccaaagcgattgccgca
ctggatggttgggtcaccgatcggtggagtacggcgggccacgatgccggggcgccgaag
ttggtggcgacggcgatcgatgccctgctcggggtggacctg

Figure 2C

MshC amino acid sequence of *M. tuberculosis* (PMshCMtP1101)

MQSWYCPPVPVLPGRGPQLRLYDSADRQVRPVAPGSKATMYVCGITPYD
ATHLGHAATYVTFDLIHRLWLDLGHELHYVQNITDIDDPLFERADRDGVD
WRDLAQAEVALFCEDMAALRVLPPQDYVGATEAIAEMVELIEKMLACGA
AYVIDREMGEYQDIYFRADATLQFGYESGYDRDTMLRLCEERGDPRRPG
KSDELDALLWRAARPGEPSWPSFPGPRPGWHVECAAIALSRIGSGLDIQG
GGSDLIFPHHEFTAHAECVSGERRFARHYVHAGMIGWDGHKMSKSRGN
LVLVSALRAQDVEPSAVRLGLLAGHYRADRFWSQQVLDEATARLHRWRT
ATALPAGPAAVDVVARVRRYLADDLTPKAIAALDGWVTDAVEYGGHD
AGAPKLVATAIDALLGVDL (SEQ ID NO: 4)

Figure 2D

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MshC amino acid sequence of *Corynebacterium striatum* (AAG03366) (PMshC-Cor.s-GB)

MHAWPDPSVPAVAGTPVPLKLFDTADQRVKEVDTPDANGEVGMVYVCGI
TPYDSTHLGHAATYLTFDLAQRQLLANGHKVHYVQNITDVDDPLFERAER
DGVDWRELGTSQINLFRSDMEILSVIPPCDYIGAMESVDEVIAMVQQLLDA
GAAYELDQGDYASIDATEQFGYESNLDRA TMEEYFAERGGDPDREGKRD
PLDALVWRGHREGEPAWDSPFGPGRPGWHVECSAIA TNRLGSHFAIQGGG
SDLAFPHHEFSAAHAEAALKVERMAGHYVHAGMIALDGVKMSKSLGNL
V FVHKLSEAGHDPSAIRLAVFAGHYREDRDFSDAILAEAEERLTRWREQL
AGEVSEAEATEVVVDKLRAILADDLNTPEALSLLDGAAGDCNQI IATA LDGL
LGVRI (SEQ ID NO: 5)

Figure 2E

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MshC amino acid sequence of *Streptomyces coelicolor* A3(2) (CAC36366)
(PMshCScGB1101)

MHAWPASEVPALPGQGRDLRIHDTATGGPVTLDPGPVARIYVCGITPYD
ATHMGHAATYNAFDLVQRVWLDTKRQVHYVQNVTDVDDPLLERAVR
DGVDWTALAEQETALFREDMTALRMLPPQHYIGAVEAIPGIVPLVERLR
DAGAAYELEGDVYFSVEADPHFGGVSHLDAATMRLLSAERGGDPDRP
GKKNPLDPMLWMAAREGEPSWDGGTLGRGRPGWHIECVAIALDHLGM
GFDVQGGGSDLAFPHHEMGASHAQALTGEFPMAKAYVHAGMVGLDG
EKMSKSKGNLVFVSQLRREGVDPAAIRLTLLAHHYRSDWEWTDQVLQ
DALARLDRWRAAVSRPDGPPAEALVEEIREALANDLDSPAALAAVDRW
AALQQESGGTDIGAPGVVSRAVDALLGVAL (SEQ ID NO: 6)

Figure 2F

8/30

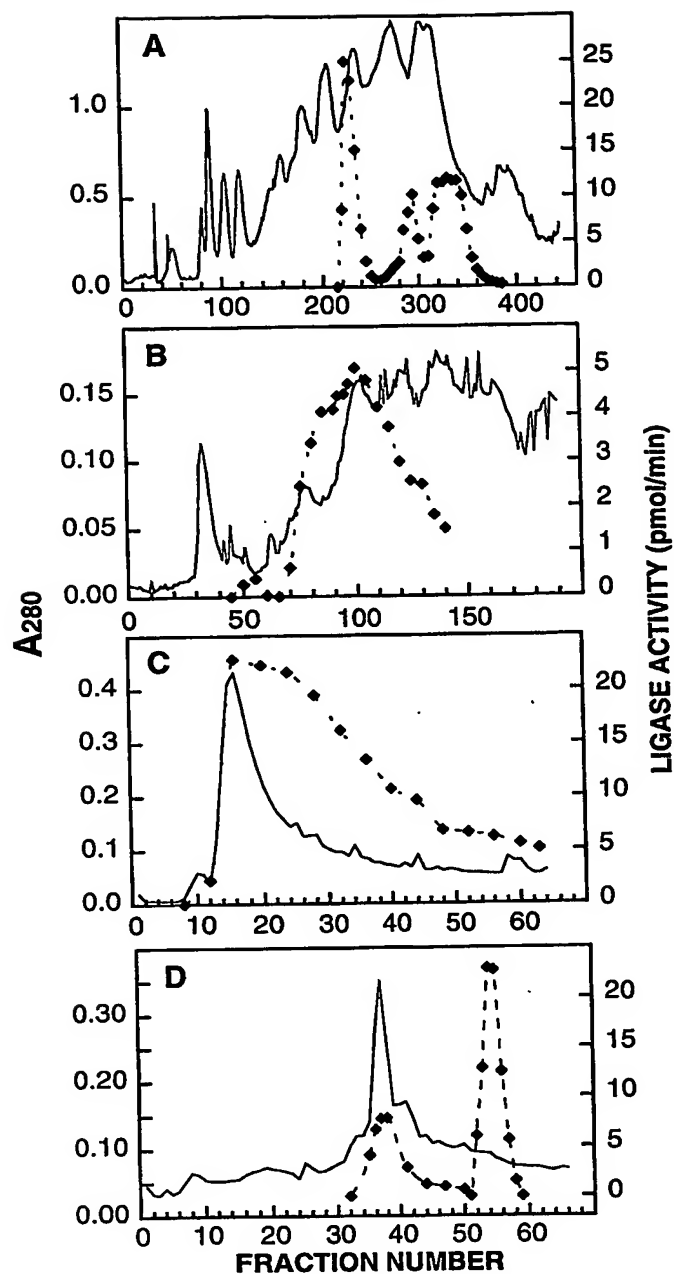


Figure 3

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	1	10	20	30	40	50	61
1. <i>M. smegmatis</i> (1)	MOSM	SAPALFVVPGRGFA	RLRLDSADROVRPV	PGPIAI	---	MYVCGITPYDATHLGHAA	
2. <i>M. tuberculosis</i> (1)	MOSMY	CEVEVLPGRGHC	RLRLDSADROVRPV	PGSKAI	---	MYVCGITPYDATHLGHAA	
3. <i>C. striatum</i> (1)	MHAMH	DESVEPAGAGTPV	PIKLFLTALQORKEVDT	TIDANGEV	CMYVCGITPYDSTHLGHAA		
4. <i>S. coelicolor</i> (1)	MHAMF	ASEVPAIPCGGRD	RLRHETATGGPV	TIDPGEVAR	---	IVVCGITPYDATHMGHAA	
	62	70	80	90	100	110	122
1. <i>M. smegmatis</i> (58)	TVLT	EDLVRLMLFAG	TVQXVONVT	TDVDDPLFERAERD	GDWRIL	GDREIQLFRDWAAL	
2. <i>M. tuberculosis</i> (58)	TVVT	EDLVRLMLDIGH	ELFYVONITL	IDDPLFERADRD	GDVDRDL	AOAEVALHCEDMAAL	
3. <i>C. striatum</i> (62)	TVLT	EDLACROTH	LANGEKHYVONIT	TDVDDPLFERAERD	GDVDRBEL	GTSOINLFRSDMET	
4. <i>S. coelicolor</i> (58)	TVTA	EDLVQRVMLD	TKRQVHYVONVT	TDVDDPLFERAVRD	GDVDMTALA	EQETALFRDWTAL	
	123	130	140	150	160	170	183
1. <i>M. smegmatis</i> (119)	RVLP	PHDYVAAD	ALAEVVEVMEKLI	ASGAAYIV	--	EDAEPPLVYFRADAT	AOFGYESCID
2. <i>M. tuberculosis</i> (119)	RVLP	EODYWGATE	ALAEWELTEKML	ACGAAYIV	IREMGEYOL	IYFRADAT	IOFGYESCYD
3. <i>C. striatum</i> (123)	SVTP	HODYIGAME	SVDFVIAW	COLLDGAAAYEL	P--	OG--	IIVASIDATEOFGYESNID
4. <i>S. coelicolor</i> (119)	RMLE	CHYVIGAVEA	IPGIVPT	VERLRDGAAYEL	EG--	---	LVYESVEADPHEGVSCHID
	184	190	200	210	220	230	244
1. <i>M. smegmatis</i> (178)	RD	TMITL	EARGGDDPR	PGKST	OLDALIMR	ADREPEPSWPS	-EFCGRPRGWHVECSAIAIT
2. <i>M. tuberculosis</i> (180)	RD	TMIRL	CEERGDDPR	PGKST	ELDALIMR	ADREPEPSWPS	-EFCGRPRGWHVECSAIAIS
3. <i>C. striatum</i> (179)	RA	MEEYFA	ERGGDDPR	EGKRLPL	DALIMRGH	REGEFAWDS	-EFCGRPRGWHVECSAIAIN
4. <i>S. coelicolor</i> (174)	AA	TMRLISA	ERGGDDPR	PGKNPL	IPMLIM	AAREBEGPSWDGGTL	GRGRPRGWHVECSAIAID
	245	250	260	270	280	290	305
1. <i>M. smegmatis</i> (238)	RIG	ICLDIQGGSDI	IFPHHE	YSAAHAE	SVTGER	RFARHYVH	IGVTCWDGHKWSKSRGNIV
2. <i>M. tuberculosis</i> (240)	RIG	SGLDIQGGSDI	IFPHHE	YSAAHAE	SVTGER	RFARHYVH	IGVTCWDGHKWSKSRGNIV
3. <i>C. striatum</i> (239)	RIG	SHPALQGGSDI	AFPHHE	YSAAHAE	AAKVER	MACHYVHAGNIA	LDGVKWSKSTGNIV
4. <i>S. coelicolor</i> (235)	HL	MGFFV	OGGSDI	AFPHHE	YV	GASHAOCAL	TGEFFPWAKAVVHAGNVCLDCEKWSKSKGNIV
	306	320	330	340	350	366	
1. <i>M. smegmatis</i> (299)	IV	SOLRAQGV	DPSAIRL	GIFSGHYRED	RFSNEVL	IDEANARI	ARMRSATVALPEAF-DATLV
2. <i>M. tuberculosis</i> (301)	IV	SALPACT	VEPSAWRL	GLIACHYRAD	REWSOOVL	IDEATARI	RMRLATAVPAQF-AAATV
3. <i>C. striatum</i> (300)	FV	HKISEA	GEDPSAIRL	AVFAGHYRED	RDFSDAIL	AEAEERL	IRMEEOIAGEVSEAEATIEV
4. <i>S. coelicolor</i> (296)	FV	SOLRREGV	DPSAIRL	TLIAHYRS	DWENTDOVI	IODALARI	IRMRAVSVREDFG-FAEAL
	367	380	390	400	410	420	
1. <i>M. smegmatis</i> (359)	IAR	VFOYL	ADDDTPK	ALALIG	CTDALS	YGGHDTES	ERLVAITVDALLGVDI
2. <i>M. tuberculosis</i> (361)	VAR	VFRYL	ADDDTPK	ALALIG	CTDALS	YGGHDTES	ERLVAITVDALLGVDI
3. <i>C. striatum</i> (361)	VDK	IFAIL	ADDDTPK	ALALIG	CTDALS	YGGHDTES	ERLVAITVDALLGVDI
4. <i>S. coelicolor</i> (356)	VEE	IFEAL	NDLSE	PAALAV	IRMAAL	LOQESGGT	LICAFGW

Figure 4

10/30

1. MshC M. tuberc. (1)	1	10	20	30	40	50	66
2. CysS M. tuberc. (1)	1	10	20	30	40	50	66
3. CysS E. coli (1)	1	10	20	30	40	50	66
1. MshC M. tuberc. (64)	67	80	90	100	110	120	132
2. CysS M. tuberc. (54)	67	80	90	100	110	120	132
3. CysS E. coli (49)	67	80	90	100	110	120	132
1. MshC M. tuberc. (130)	133	140	150	160	170	180	198
2. CysS M. tuberc. (120)	133	140	150	160	170	180	198
3. CysS E. coli (115)	133	140	150	160	170	180	198
1. MshC M. tuberc. (196)	199	210	220	230	240	250	264
2. CysS M. tuberc. (177)	199	210	220	230	240	250	264
3. CysS E. coli (175)	199	210	220	230	240	250	264
1. MshC M. tuberc. (262)	265	270	280	290	300	310	330
2. CysS M. tuberc. (240)	265	270	280	290	300	310	330
3. CysS E. coli (238)	265	270	280	290	300	310	330
1. MshC M. tuberc. (328)	331	340	350	360	370	380	396
2. CysS M. tuberc. (303)	331	340	350	360	370	380	396
3. CysS E. coli (302)	331	340	350	360	370	380	396
1. MshC M. tuberc. (390)	397	410	420	430	440	450	462
2. CysS M. tuberc. (369)	397	410	420	430	440	450	462
3. CysS E. coli (368)	397	410	420	430	440	450	462
1. MshC M. tuberc. (434)	463	470	480	498			
2. CysS M. tuberc. (431)	463	470	480	498			
3. CysS E. coli (431)	463	470	480	498			

Figure 5

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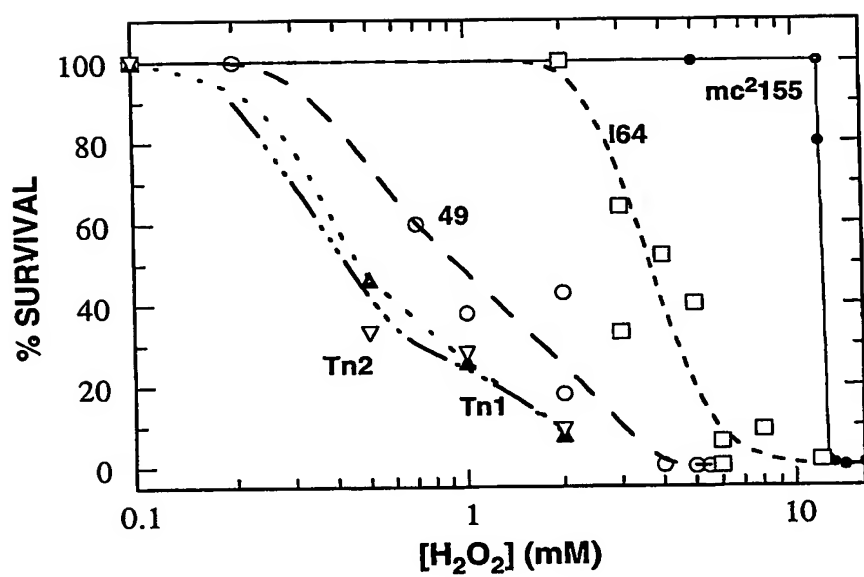
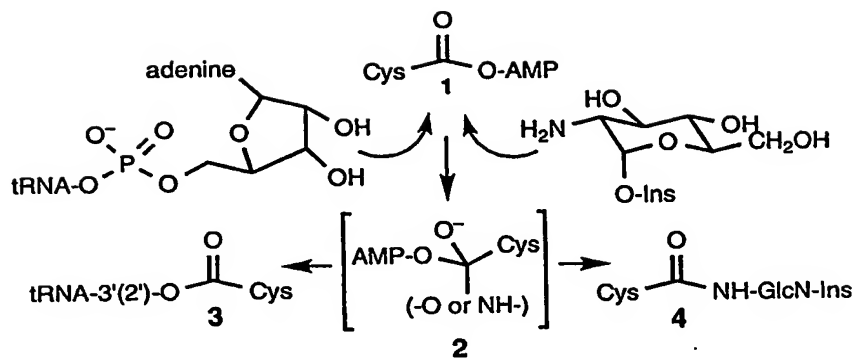


Figure 6

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**Figure 7**

13/30

		1		50					
<i>M. tuberculosis</i>	(1)	-----VTALDWRSA	LTAD	EQRSVRALVTATTAVDGVAPVGEQV-					
<i>M. smegmatis</i>	(1)	-----VTSTEWRTGLT	GACQAEIRALID	AATHDGVAPVGDQV-					
<i>M. leprae</i>	(1)	-----MVLNWRFA	LSADEQRLVREI	ISAATEFDEVPVGEQV-					
<i>S. coelicolor</i>	(1)	MTSDDTVRPGRP	RSIETLAE	LTP	EQTD	AVLALLTEAARTDGOHAVSEQGR			
<i>C. diphtheriae</i>	(1)	-----MIETSLAS	ASAAALRDRV	DEILAAATREDGCAPLSE	SFL				
		51		100					
<i>M. tuberculosis</i>	(39)	--LRELQOORTEH	LLVAGSRPGCE	IIIGYLNLSPPRCAGG	AMAE	LVVHPQS			
<i>M. smegmatis</i>	(39)	--LRELGRDRTR	HLLLTDD---	DRVVGYLNLA	PAEGOD	PAMAE	LVVHPQA		
<i>M. leprae</i>	(38)	--LRELGYDRTE	HLLVTD	SRPYAIIIGYLNLS	SPRDAG	VAMAE	LVVHPRE		
<i>S. coelicolor</i>	(51)	LQLRGPA	REGVVHLLLTLD	--GGELVGYA	QLEG	TD	PVEPPAE	LVVHPSH	
<i>C. diphtheriae</i>	(39)	NGLRR-ADD	GHVHSCVMS	--HDQVVG---	VAARDGDS---	AEVVVD	PAF		
								pfam00583-	
		101		150					
<i>M. tuberculosis</i>	(87)	RRRGIGTAMARA	ALAKTAGRNQ	FWAHGTLDP	PARATASAL	GLVGV	REL	IQM	
<i>M. smegmatis</i>	(84)	RRRGIGAAMAR	TALAE	EGGPGARI	WAHCNIAAAQ	AMASSRL	LVV	VRELLQM	
<i>M. leprae</i>	(86)	RRRGVGAAMV	RAALAKTG	CNRNFWAHG	TLASARATAS	VLGLVP	VREL	VQM	
<i>S. coelicolor</i>	(99)	RGCGHGRALG	SALLAASG	KRLRIWAH	GGHSAARHLA	QVLGL	SLF	RELROL	
<i>C. diphtheriae</i>	(80)	RRQGYGSFLI	RHVVSQGVKN	--VWAHGD	GAGAKAVAKA	LOLE	QTR	OLLVM	
		151		200					
<i>M. tuberculosis</i>	(137)	RRPL-R--DI	PEPTIPD--	GVVI---	RTYAGTSD-	DAEL	LRV	NNAAFAG	
<i>M. smegmatis</i>	(134)	RRPL-T--DL	P-P--VPD	TGVR---	ATYAGPGD-	DAEL	LRV	NNAAFSW	
<i>M. leprae</i>	(136)	QRSL-R--T	IPDPMPD	QLGVWV---	RTYVGTVD-	DAEL	LRV	NNAAFAG	
<i>S. coelicolor</i>	(149)	RRPL-TGL	DLPEPRI	PE--GVS	V---RTF	VPGQD-	DAAW	LAVNAAFAH	
<i>C. diphtheriae</i>	(128)	AVEGDR	LIVESAQ	LQVPS--	GFRVLAL	NEAVESIP	DIEQ	QWLRVNNEAF	
		201		250					
<i>M. tuberculosis</i>	(177)	HPEQGGWTA	VQLAERR	CEAWF--	DPDGLILAF	GDS	SPRER	PGRL	LLGFHWTKV
<i>M. smegmatis</i>	(174)	HPEQGGWTE	HEIDER	RNEGWF--	DPEGLFO	AFD---	EQTGS	LLGFHWTKI	
<i>M. leprae</i>	(178)	HPEQGGWTAT	QLAERR	SEPWF--	DPAGLFLAF	GDS	SSNO	PGKIL	LLGFHWTKV
<i>S. coelicolor</i>	(191)	HPEQGSILT	QRDLDD	RKAEPWF--	DPAGFFLA	-----	ERDGE	LIGFHWTKV	
<i>C. diphtheriae</i>	(176)	HPEQGGWDS	ARLAQARD	TQWFER	SDVLF	FLID----	TAKRT	VAGFHWTKR	
		251		300					
<i>M. tuberculosis</i>	(226)	HPD--HPGL	GEVYVLG	VDPA	AQRRGLG	QMLT	SIGIV	SLARR	LGGRKTLDP
<i>M. smegmatis</i>	(219)	HD---ASL	GEVYVLG	VDPA	QGRGLG	YTLTL	LIGL	HHLA	EKLAG----
<i>M. leprae</i>	(227)	HAA--HPGL	GEVYVLG	VDPS	AQGRGLG	QMLT	SIGIAS	LAQR	LVG----
<i>S. coelicolor</i>	(234)	HA---EER	LGEVYVLG	IRPDT	QGGGLG	KALTT	LGLRH	LEGQ--	G-----
<i>C. diphtheriae</i>	(221)	HGD	LAEGAD	GEVYV	GLGSAYRR	RGLGDL	LIRM	GLHH	LEYEHAR----
									pfam00583-
		301		343					
<i>M. tuberculosis</i>	(274)	AVEPAVLL	YVESDN	VAAV	RTYQSLG	FTTYS	VD	TAYAL	AGTDN--
<i>M. smegmatis</i>	(260)	--EPTV	LLYVEAD	NSAAV	NTYRK	LGFEV	FSDA	AYAN	----
<i>M. leprae</i>	(270)	SAEPTV	MLYVES	DNVAA	ARTYER	L	GFTTYS	VD	TAYALARIDD-
<i>S. coelicolor</i>	(273)	--LPTA	MLYVDAD	NKAAV	VYER	L	GFVTH	ETDL	MYRTET----
<i>C. diphtheriae</i>	(265)	--R--VIL	YVEGD	NESARRA	YDAL	LG	FHV	ESHV	TSPOSSS--

Figure 8

14/30

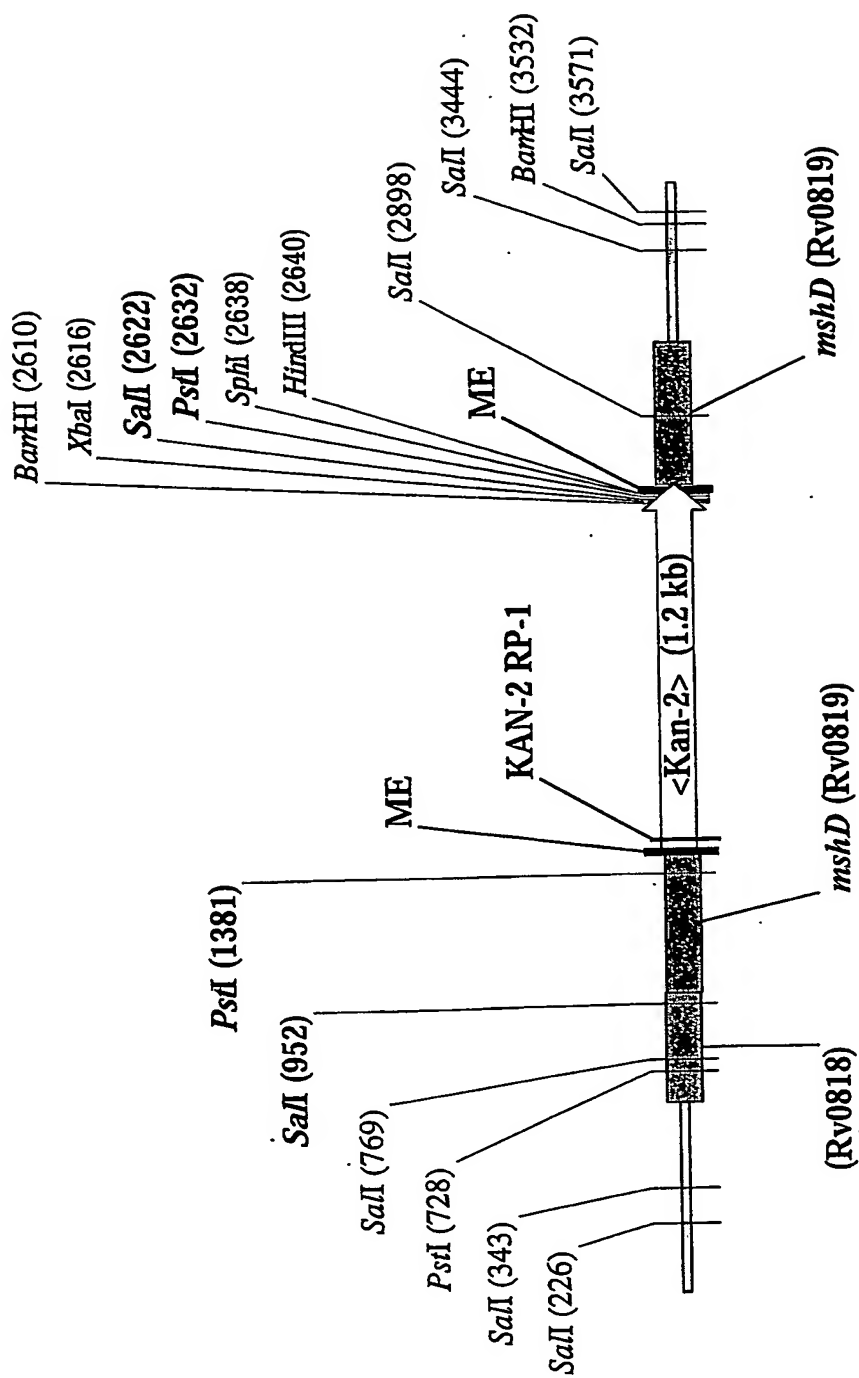


Figure 9

15/30

MshD amino acid sequence of *M. tuberculosis* (CAA17625.1) (Rv0819)

MTALDWRSALTAEQRSVRALVTATTAVDGVAPVGEQVLRELGQQRT
EHLVAGSRPGGPPIIGYLNLSPPRGAGGAMAELVVHPQSRRRGIGTAMA
RAALAKTAGRNQFWAHGTLDPARATASALGLVGVRELIQMRRPLRDIP
EPTIPDGVVIRTYAGTSDDAELLRVNNAAFAGHPEQGGWTAVQLAERR
GEAWFDPDGLILAFGDSPRERPGRLLGFHWTKVHPDHPGLGEVYVLGV
DPAAQRRGLGQMLTSIGIVSLARRLGGRKTLDPAVEPAVLLYVESDNVA
AVRTYQSLGFTTYSVDTAYALAGTDN (SEQ ID NO: 14)

Figure 10A

16/30

MshD amino acid sequence of *M. smegmatis* (PMshDMs-Tr)

VTSTEWRTGL TGAQQAEIRA LIDAATTHDG VAPVGDQVLR
ELGRDRTRHL LTTDDDRVVG YLNLAPAEGD DPAMAELVVH
PQARRRGIGA AMARTALAEG GPGARIWAHG NIAAAQAMAS
SLRLVVVREL LQMRRPLTDL PPVPDTPGVR IATYAGPGDD
AEILRVNNAA FSWHPEQGGW TEHEIDERRN EGWFDPEGLF
QAFDEQTGSL LGFHWTKIHD ASLGEVYVVG VDPQAQGRGL
GYTLTLIGLH HLAEKLAGPE PTVLLYVEAD NSAAVNTYRK
LGFEVFSVDA AYAAN (SEQ ID NO: 15)

Figure 10B

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MshD amino acid sequence of *M. leprae* (ML2193)

MVLNWRFALESADEQRLVREIISAATEFDEVSPVGEQVLRELGYDRTEHL
LVTDSRPYAPIIGYLNLSRPDAGVAMAELVVHPRERRRGVGAAMVRA
ALAKTGGRNRFWAHGTLASARATASVLGLVPVREL VQMQRSLRTIPDP
MVPDQLGVWVRTYVGTVDDAELLRVNNAAFAGHPEQGGWTATQLAE
RRSEPWFDPAFLAFLAGDSSSNQPGKLLGFHWTKVHAAHPGLGEVYVL
GVDPSAQGRGLGQMLTSIGIASLAQRLVGPSAEPTVMLYVESDNVAAA
RTYERLGFTTYSVDTAYALARIDD (SEQ ID NO: 16)

Figure 10C

18/30

MshD amino acid sequence of *Streptomyces coelicolor* (SCD84.18c, SCO4151)

MTSDDTVRPGRPRSIETLAELTPEQTDVLAALLTEAARTDGQHAVSEQG
RLQLRGPAAREGVVHLLLTLDGGELVGYAQLEGTDPEPPAAELVVHPS
HRGQGHGRALGSALLAASGKRLRIWAHGGHSAARHLAQVLGLSLFREL
RQLRRPLTGLDLPEPRLPEGVSVRTFVPGQDDAAWLAVNAAFAHHPE
QGSLTQRDLDDRKAEPWFDPAGFFLAERDGELIGFHWTKVHAEERLGE
VYVLGIRPDTQGGGLGKALTTIGLRHLEGQGLPTAMLYVDADNKAAVA
VYERLGFVTHETDLMYRTET (SEQ ID NO: 17)

Figure 10D

19/30

MshD amino acid sequence of *Corynebacterium diphtheriae* (PMshDCd-Tr)

MIETSLASAS AALRDRVDEI LAAATREDGC APLSESFLNG
LRRADDGHVH SCVMDSHDQV VGVAARDGDS AEVVVDPAFR
RQGYGSFLIR HVVSQGVKNV WAHGDGAGAK AVAKALQLEQ
TRQLLVMAVE GDRLVESAQL QVPSGFRVLA LNEAYESIPD
IEQQWLRVNN EAFEWHPEQG GWDSARLAQA RDTQWFRES
VLFLIDTAKR TVAGFHWTKR HGDLAEGADG EVYVVGLGSA
YRRRGLGDLL IRMGLHHLEY EHARRVILYV EGDNESARRA
YDALGFHVVE SHVTYSPQSS S (SEQ ID NO: 18)

Figure 10E

20/30

Nucleic acid sequence *mshD* *M. smegmatis*, including stop codon

GTGACCTCCACCGAGTGGCGCACCGGGCTCACGGGTGCCCAGCAGG
CAGAGATTCGCGCGCTGATCGACGCGGCCACACGCACGACGGTGT
CGCGCCGGTCGGTGACCAAGTGCTGCGGGAAC TGGGACGCGACCGC
ACCGGGCACCTGCTGACCACCGACGACGACCGCGTGGTCGGATACCT
CAACCTCGCGCCTGCCGAGGGGGACGATCCGGCGATGGCCGAAC TC
GTCGTGCATCCGCAGGCCCGCCGGCGCGGTATCGGTGCGGCCATGGC
GCGCACCGCGCTGGCAGAGGGCGGGGCCGGGCGCCCGTATCTGGGCG
CACGGCAACATCGCCGCCGCCAGGCGATGGCGTCATCGCTTCGCCT
GGTGGTGGTGCCTGAGCTGCTGCAGATGCGCCGCCCCCTGACCGATC
TGCCGCCGGTGCCGGACACCCCCGGCGTGCGCATCGCGACCTACGCC
GGCCCCGGCGACGACGCCGAGATCCTGCGGGTCAACAACGCCGCGT
TCTCGTGGCACCCCGAGCAGGGCGTGA (SEQ ID NO: 48)

Figure 10F

21/30

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MshA-Msmeg 1-----VRLATDLET PRRVAVLSVHTSPLAQPGTGDA 1-
MshA-Mtub 1MAGVRHDDGSLIAQRRPVRGEGATRSRGPSPGSPNENVSAADDPRRVALLAVHTSPLAQPGTGDA
SpsA-Anab 1-----MFQNKKHRIALISVSGDPAVEICQEEA
PimB-Mtub 1-----VCGVRVAIVAESFLPQVN-----
          *-BOX I--|
MshA-Msmeg 32GGMNVYVLQATALQLARRGV E V E V F T R A T S S A D A P V V P V A P G V L V R N V V A G P F E G L D K N D L P T Q L C
MshA-Mtub 66GGMNVYMLQSALHLARRGIEVEITFTRATASADFPVVRVAPGV LVRNVVAGPFEGLDKYDLPTQLC
SpsA-Anab 28GGQNVYVREVG YALAEQGWQVDMETRRISPDQAEIVQHS PNCRTIRLQAGPVEFIFGRDHVFDYLP
PimB-Mtub 19-GVSN SVVKVLEHLRRTCHEALVIAPDTPPGEDRAERLHDGVRVHRVPSRMFPKVT--TLELGVP

MshA-Msmeg 97AFTAGVLR AEATHEPGY-YDVVHSHY-WLSGQVGWLARDRWAVPLVHTAHTLA AVKNAALAAAGDA
MshA-Mtub 131AFAAGVLR AEAVHEPGY-YD TVHSHY-WLSGQVGWLARDRWAVPLVHTAHTLA AVKNAALADGDG
SpsA-Anab 93EFVAEFQRFQK--RQGYNYQLIHTNY-WLSSWVGMLKKQQLV L VHTYHSLGAIKYQTIA--DI
PimB-Mtub 81TFR--MLRALR----GFDPDVVHLASPA LLGYGGLHAARRLG VETVAVYQTDVPGFASSYG---I
                                     G242↓ ↓D244
MshA-Msmeg 160PEPPLRAVGEQQQVDEADRLIVNTEVEAQQLVSLHNADRSRIDV VHPGVLDLVETPGSRDAARAV
MshA-Mtub 194PEPPLRTVGEQQVDEADRLIVNTDDEARQVISLHGADPARIDV VHPGVLDLVETPGDRRAARAA
SpsA-Anab 153PAIANQRLAIEKACLESVDTVVATSPQEQQHMRALVSKKGRIEMI PCGTDINNEGNI EKSAAREK
PimB-Mtub 137PMTARA AWA WFRHLHRLADRTLAPSTATMESLIAQGIP--RVHRWARGVDVQREAF SARNEVLRR
                                     R273↓ ↓K278
MshA-Msmeg 225EGLEPTDOKIVAFVVGRIQPLKAPDILLRAAAK-----LPGVRVLIAGG--PSGSGLAOPDTLVRLA
MshA-Mtub 259LGLEVDERVAFVVGRIQPLKAPDIVLRAAAK-----LPGVRIIVAGG--PSGSGLASPDGLVRLA
SpsA-Anab 218LGIEPDAMVFYVGRFDPKGIETLVRAVAQSR LRGEANLQLVIGGSRFQGS DGRERDRIANIV
PimB-Mtub 200RWS E D G K P I V G F V G R L A P E K H V U R L T G L A A S -----GAVRLVIVG-----DGIDFAR
                                     E354↓-----BOX II-----|
MshA-Msmeg 283DELGISDRVTFLPPQSREQLVNVYRAADLVAVPSYSESFGLVAVEAQACGTPVVA AVVGGLPVAV
MshA-Mtub 317DELGISARVTFLPPQSH TDLATLFRAADLVAVPSYSESFGLVAVEAQACGTPVVA AVVGGLPVAV
SpsA-Anab 283AELELNDCTTFAGRLDHEILPYYIAAADVCVVP SHYEPFGLVATEAMASKTPV IASNVGGLQFTV
PimB-Mtub 247LQSAMPT-AVETGARYGKELAEAYASMDV FVHSGEHETFCQVVOEALASGLPV IAPDAGGPRDLI

MshA-Msmeg 348ADGVSGALVD-GHDIGDWADTI SEVLDREPA----ALSRASAEHAAQFSWAHTV DALLASYSRAM
MshA-Mtub 382RDGTTGTLVS-GHEVGOWADAIDHLLRLCAGPRGRVMSRAAARHAATFSWENTTDALLASYRRAI
SpsA-Anab 348VPEVTGLLAP-PQDESAFATAIDRILANPTWR-DQLGTAARQ RVETTFSWAGVASOLSQLYTHLL
PimB-Mtub 311TPHRTGLLL PVGEFEHRLPDAVAHLVHERQR----YALAAARRSVLGRSWPVVCD ELLGHYEAVR

MshA-Msmeg 408SDYRARHPRPA-----ARRSGRRFSMRRGVRT
MshA-Mtub 446GEYNAERQRRGGEVISDLVAVGKPRHWTFRRGVGA
SpsA-Anab 411TONAPEKKEKE-----AVAA-----
PimB-Mtub 371GRRTTQAA-----

```

Figure 11

22/30

MshA amino acid sequence of *M. smegmatis* (PMshAMs-Tr)

VRLATDLETP RRVAVLSVHT SPLAQPGTGD AGGMNVYVLQ
TALQLARRGV EVEVFTRATS SADAPVVPVA PGVLVRNVVA
GPFEGLDKND LPTQLCAFTA GVLRAEATHE PGYYDVVHSH
YWLSGQVGWL ARDRWAVPLV HTAHTLAAVK NAALAAGDAP
EPPLRAVGEQ QVVDEADR LI VNTEVEAQQL VSLHNADRSR
IDVVHPGV DL DVFTPGSRDA ARAVFGLPTD QKIVAFVGRI
QPLKAPDILL RAAAKLPGVR VLIAGGPSGS GLAQPD TLVR
LADELGISDR VTFLPPQSRE QLVNVYRAAD LVAVPSYSES
FGLVAVEAQA CGTPVVAAAV GGLPVAVADG VSGALVDGHD
IGDWADTISE VLDREPAALS RASAEHAAQF SWAHTVDALL
ASYSRAMSDY RARHPRPAAR RSGRRFSMRR GVRT (SEQ ID NO: 19)

Figure 12A

23/30

MshA amino acid sequence of *M. tuberculosis* (PMshAMtG1002)

MAGVRHDDGS GLIAQRRPVR GEGATRSRGP SGPSNRNVSA
ADDP RR VALL AVHTSPLAQP GTGDAGGMNV YMLQSALHLA
RRGIEVEIFT RATASADPPV VRVAPGVLVR NVVAGPFEG
LDKYDLPTQLC AFAAGVLRAE AVHEPGYYDI VHSHYWLSGQ
VGWLARDRWA VPLVHTAHTL AAVKNAALAD GDGPEPPLRT
VGEQQVVDEA DRLIVNTDDE ARQVISLHGA DPARIDVVHP
GVDLDVFRPG DRRAARAALG LPVDERVVA FVGRIQPLKAP
DIVLRAAAKL PGVRIIVAGG PSGSGLASPD GLVRLADELG
ISARVTFLPP QSHTDLATLF RAADLVAVPS YSESFGLVAV
EAQACGTPVV AA AVGGLPVA VRDGITGTLV SGHEVGQWAD
AIDHLLRLCA GPRGRVMSRA AARHAATFSW ENT TDALLAS
YRRAIGEYNA ERQRRGGEVI SDLVAVGKPR HWTPRRGVGA (SEQ ID
NO: 20)

Figure 12B

24/30

Nucleic acid sequence *mshA* *M. smegmatis*, including stop codon

GTGCGTCTAGCGACAGACCT
CGAGACCCCCCGCCGCGTGGCGGTGTTGTCGGTACACACCTCTCCGC
TGGCGCAGCCGGGCACCGGCGACGCGGGCGGCATGAACGTCTACGT
GTTGCAGACCGCGCTGCAACTGGCCCCGGCGTGGCGTCGAGGTCGAG
GTCTTCACCAGGGCCACGTCGTCGGCCGATGCGCCGGTTCGTGCCTGT
GGCGCCCCGGTGTGCTGGTGC GCAACGTCGTGGCCGGCCCCGTTCTGAAG
GCCTCGACAAGAACGATCTGCCACGCAGCTGTGCGCGTTTACC GCG
GGTGTGCTGCGCGCCGAGGCGACCCACGAGCCCCGGCTACTACGACG
TCGTGCATTTCGCACTACTGGCTGTCCGGCCAGGTCGGGTGGCTGGCG
CGCGACCGCTGGGCCGTGCCGCTGGTGCACACCGCGCACACGCTGG
CCGCGGTCAAGAACGCCGCACTCGCCGCGGGCGACGCACCCGAGCC
GCCGCTGCGCGCGGTGGGCGAACAACAGGTGGTCGACGAGGCCGAC
CGCCTCATCGTGAACACCGAAGTCGAAGCGCAGCAACTGGTCTCGTT
GCACAATGCCGACCGCTCACGCATCGACGTCGTGCACCCCGGCGTCG
ATCTCGACGTGTTTACCCCCGGTTCGCGCGACGCGGCGCGCGCGGTG
TTCGGGCTTCCCACCGACCAAGAAGATCGTGGCGTTCGTGGGCCGCAT
CCAGCCGCTCAAGGCCCGGACATCCTGCTGCGTGCCGCGGGCGAAAC
TGCCCGGCGTGCGCGTGCTGATCGCCGGTGGACCCTCCGGATCGGGA
CTTGCCCAACCGGACACGCTGGTTCGGCTCGCCGACGAAC TGGGTAT
CAGTGACCGGGTGACGTTCTCCCGCCGACAGCCGCGAACA ACTG
GTCAACGTGTACCGGGCGGGCCGATCTGGTCGCGGTGCCGAGCTACTC
CGAGTCGTTTCGGCCTGGTTCGCCGTCGAGGCGCAGGCGTGCGGCACGC
CCGTCGTCGCCGCGGGCCGTCCGGCGGACTGCCGGTCGCGGTGGCCGAC
GGCGTCAGCGGGGCACTCGTCGACGGCCACGACATCGGCGACTGGG
CCGACACCATCAGCGAGGTGCTCGACCGCGAGCCCGCCGCGCTGAG
CCGCGCCTCCGCCGAACACGCCGCTCAGTTCTCGTGGGCGCACACCG
TCGACGCGCTGCTCGCCAGCTACAGCCGGGCCAT
GAGTGACTACCGGGCCCGTCATCCCAGACCCGCCGCGCGGGCGTTCCG
GACGCCGGTTCTCGATGCGCAGGGGAGTACGCACGTGA (SEQ ID NO:
49)

Figure 12C

25/30

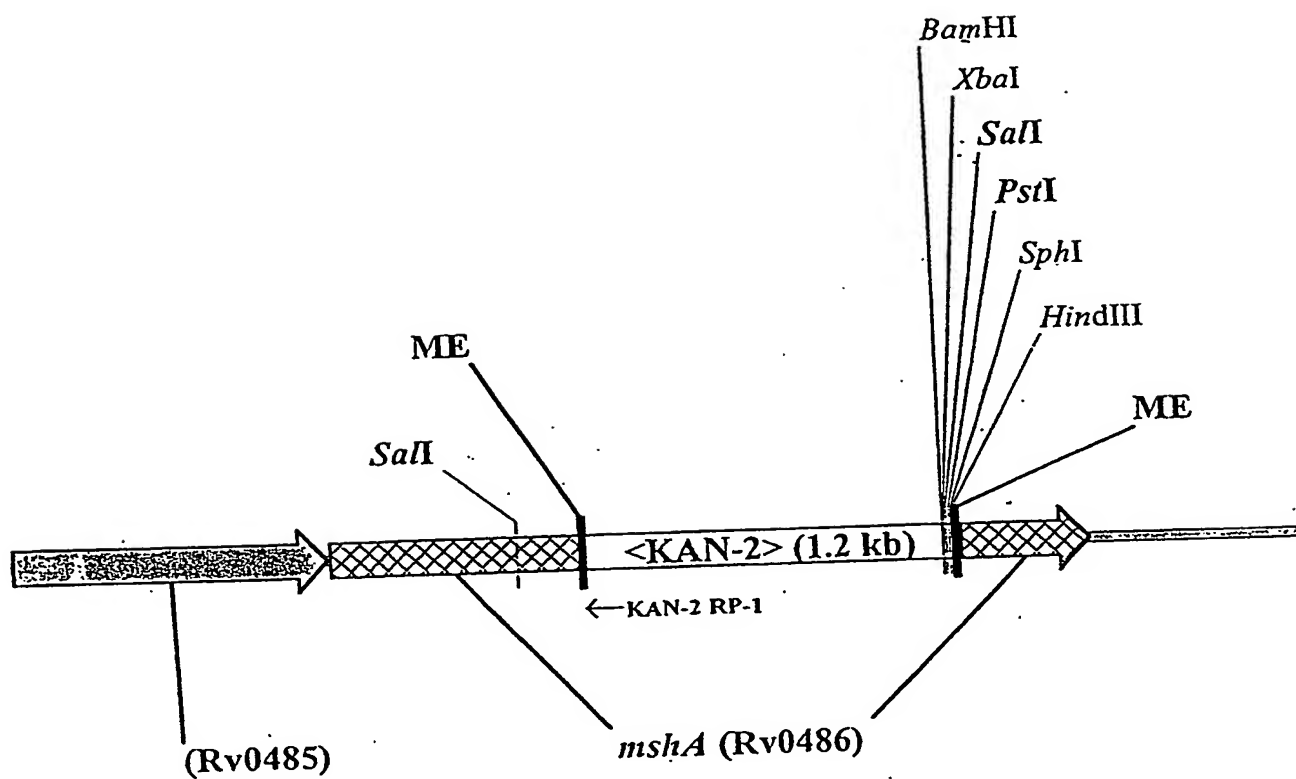


Figure 13

26/30

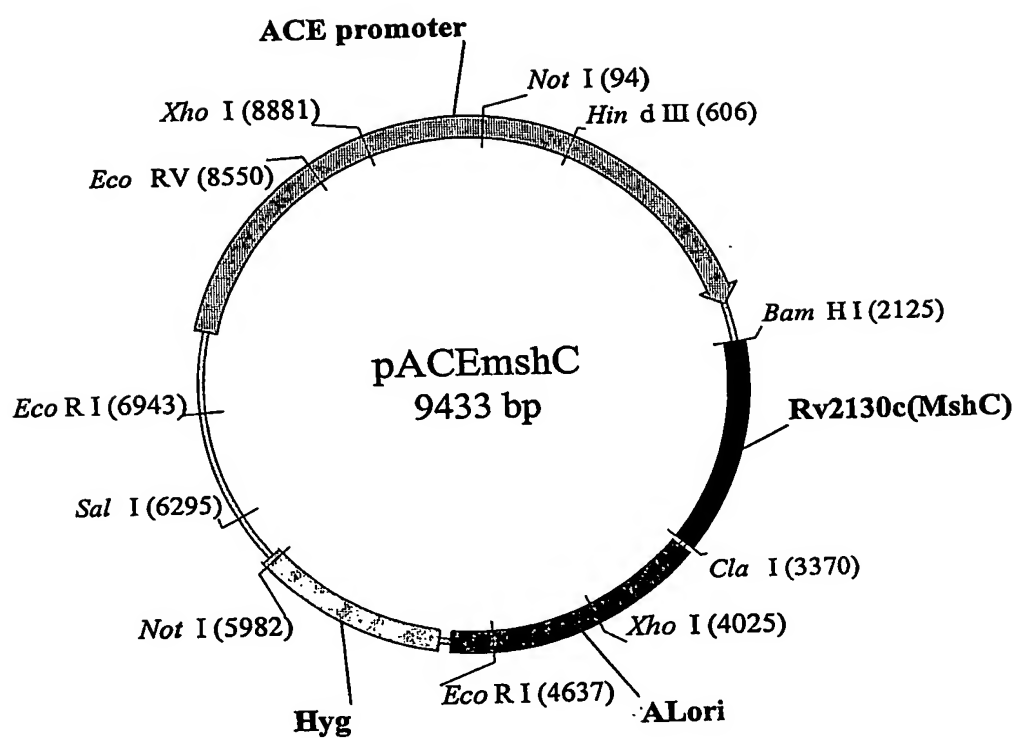


Figure 14

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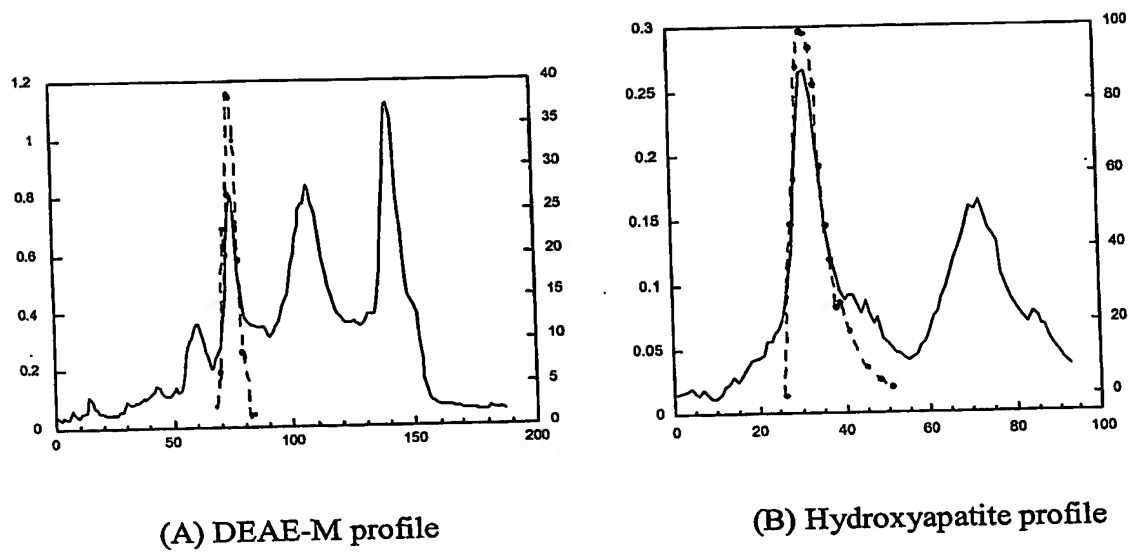
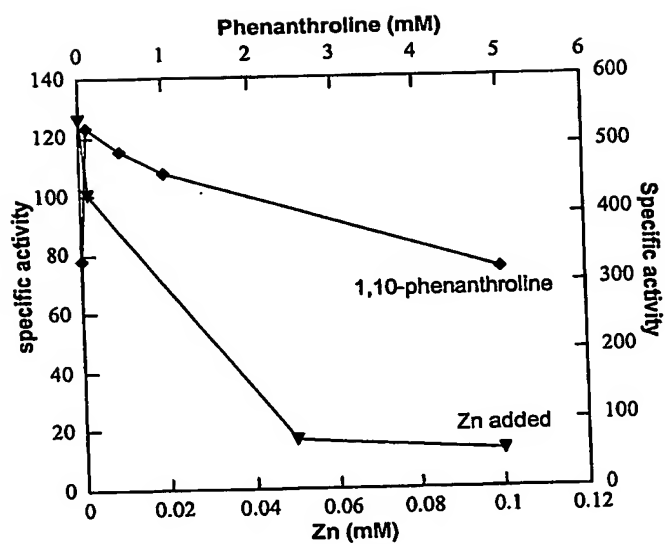


Figure 15

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**Figure 16**

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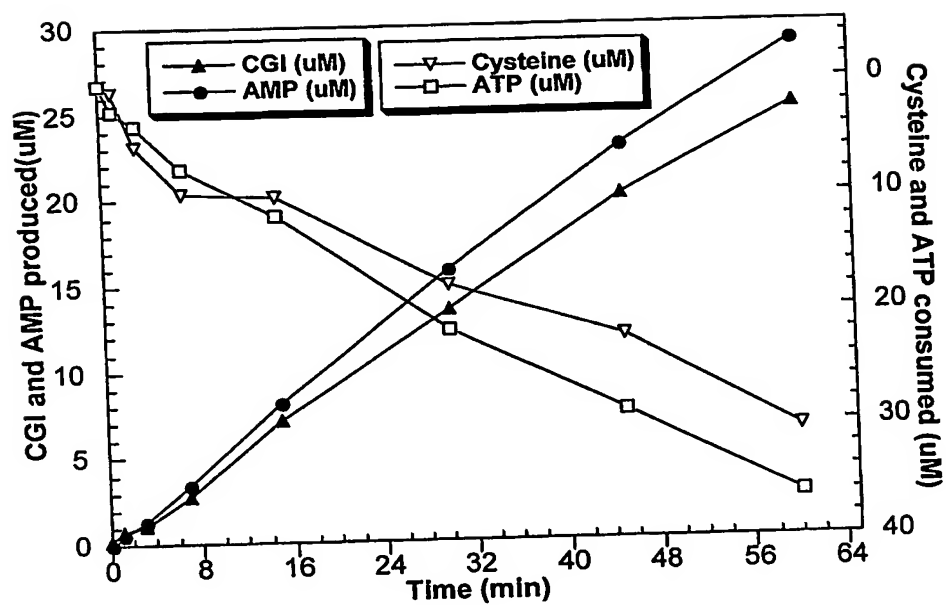


Figure 17

30/30

(a) First Half of Rossman fold:

M. smeg MshC (40) --MYVCGITPYDATHLGHAAATYLTFDL (64)
M. lepr Mshc (11) ATMYVCGITPYDATHLGHAAATYLAFDL (37)
S. coel. MshC (40) --IYVCGITPYDATHMGHAAATYNAFDL (64)
C. strt. MshC (44) --MYVCGITPYDSTHLGHAAATYLTFDL (68)
T. bifu. MshC (40) --MYVCGITPYDAAHLGHAAATYLTFDL (64)
M. tubr Cyss (30) --IYLCGATVQGLPHIGHVRSGVAFDI (54)
E. coli Cyss (25) --MYVCGITVYDLCHIGHGRTEFVAFDV (49)

(b) Second half of Rossman Fold:

M. smeg MshC (218) SPFGRRPGWHEVECSAIALTRIGTGLDIQGGGSDLIFFPHHEYSAHAESVT
M. lepr MshC (190) SPFGRRPGWHEVECAIALSRIGIGLDIQGGGSDLIFFPHHEFTAAHAECVR
S. coel. MshC (215) GTLGRGRPGWHEIEVAIALDHLGMGFDVQGGGSDLAFFPHHEMGASHAQALT
C. strt. MshC (219) SPFGRRPGWHEVECSAIALNRLGSHFAIQGGGSDLAFFPHHEFSAAHAEAL
T. bifu. MshC (198) TPLGRGRPGWHEVECSAISVHELGMGFDLNGGGDDLIFFPHHEMGAAEACCAT
M. tubr Cyss (214) TPWGRGRPGWHELECSAMARSYLGPFDIHC GGMDLVFPHEHENEIAQSRAAG
E. coli Cyss (196) SPWGAGRRPGWHEIECSAMNCKQLGNHFDIHGGGSDLMFPHEHENEIAQSTCAH

M. smeg MshC GERREARHYVHTGMIGWDGHKMSKS (293)
M. lepr Mshc GERREARHYVHAGMIGWDEHKMSKS (265)
S. coel. MshC GEFPMAKAYVHAGMVGLDGEKMSKS (290)
C. strt. MshC KVERMAGHYVHAGMIALDGVKMSKS (294)
T. bifu. MshC GSRPQARHYLHVAMVGLDGEKMSKS (289)
M. tubr Cyss DG--FARYWLHNGWVTMGGEKMSKS (271)
E. coli Cyss DGQ-YVNYWMHSGVMVMDREKMSKS (270)

Figure 18

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